#2

RAW SEQUENCE LISTING   DATE: 12/12/2001
PATENT APPLICATION: US/10/003,919   TIME: 14:26:26

Input Set : A:\RTS-0256 Sequence Listing.txt **ENTERED**
Output Set: N:\CRF3\12112001\I003919.raw

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   6 <110> APPLICANT: C. Frank Bennett
   7         Susan M. Freier
   9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
  11 <130> FILE REFERENCE: RTS-0256
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/003,919
C--> 13 <141> CURRENT FILING DATE: 2001-12-06
  13 <160> NUMBER OF SEQ ID NOS: 87
  16 <210> SEQ ID NO: 1
  17 <211> LENGTH: 20
  18 <212> TYPE: DNA
  19 <213> ORGANISM: Artificial Sequence
  21 <220> FEATURE:
  23 <223> OTHER INFORMATION: Antisense Oligonucleotide
  25 <400> SEQUENCE: 1
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  29 <210> SEQ ID NO: 2
  30 <211> LENGTH: 20
  31 <212> TYPE: DNA
  32 <213> ORGANISM: Artificial Sequence
  34 <220> FEATURE:
  36 <223> OTHER INFORMATION: Antisense Oligonucleotide
  38 <400> SEQUENCE: 2
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  42 <210> SEQ ID NO: 3
  43 <211> LENGTH: 5273
  44 <212> TYPE: DNA
  45 <213> ORGANISM: Homo sapiens
  47 <220> FEATURE:
  49 <220> FEATURE:
  50 <221> NAME/KEY: CDS
  51 <222> LOCATION: (513)...(4079)
  53 <400> SEQUENCE: 3
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  56 cacccatgcc tgctaggcca tgcttcttca gaagtggcca caactctcct gacgtctcca  120
  58 gagccggtca ttccacccag ggggacttca gctgccactg gacacttcaa ttgtacgctg  180
  60 cgaccagttg ccaggaagga gagggctggc aagaaagccg cggcagccgt ggcagggtgt  240
  62 atgggacggt ggacggccag ggcccccccc tctctctctt tctctctctc tctcttgctt  300
  64 ggtttctgta atgaggaagt tctccgcagc tcagtttcct ttccctcact gagcgcctga  360
  66 aacaggaagt cagtcagtta agctggtggc agcagccgag gccaccaaga ggcaacgggc  420
  68 ggcaggttgc agtggagggg cctccgctcc cctcggtggt gtgtgggtcc tggggtgcc  480
  70 tgccggccca gccgaggagg cccacgccca cc atg gtc ccc tgc tgg aac cat  533
  71                                   Met Val Pro Cys Trp Asn His
  72                                    1               5
  74 ggc aac atc acc cgc tcc aag gcg gag gag ctg ctt tcc agg aca ggc  581
  75 Gly Asn Ile Thr Arg Ser Lys Ala Glu Glu Leu Leu Ser Arg Thr Gly
  76          10              15              20
  78 aag gac ggg agc ttc ctc gtg cgt gcc agc gag tcc atc tcc cgg gca  629
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79 Lys Asp Gly Ser Phe Leu Val Arg Ala Ser Glu Ser Ile Ser Arg Ala
80      25                      30              35
82 tac gcg ctc tgc gtg ctg tat cgg aat tgc gtt tac act tac aga att     677
83 Tyr Ala Leu Cys Val Leu Tyr Arg Asn Cys Val Tyr Thr Tyr Arg Ile
84  40                      45              50                  55
86 ctg ccc aat gaa gat gat aaa ttc act gtt cag gca tcc gaa ggc gtc     725
87 Leu Pro Asn Glu Asp Asp Lys Phe Thr Val Gln Ala Ser Glu Gly Val
88                  60                  65                  70
90 tcc atg agg ttc ttc acc aag ctg gac cag ctc atc gag ttt tac aag     773
91 Ser Met Arg Phe Phe Thr Lys Leu Asp Gln Leu Ile Glu Phe Tyr Lys
92              75                  80                  85
94 aag gaa aac atg ggg ctg gtg acc cat ctg caa tac cct gtg ccg ctg     821
95 Lys Glu Asn Met Gly Leu Val Thr His Leu Gln Tyr Pro Val Pro Leu
96              90                  95                  100
98 gag gaa gag gac aca ggc gac gac cct gag gag gac aca gaa agt gtc     869
99 Glu Glu Glu Asp Thr Gly Asp Asp Pro Glu Glu Asp Thr Glu Ser Val
100     105                     110                 115
102 gtg tct cca ccc gag ctg ccc cca aga aac atc ccg ctg act gcc agc    917
103 Val Ser Pro Pro Glu Leu Pro Pro Arg Asn Ile Pro Leu Thr Ala Ser
104 120                     125                 130                 135
106 tcc tgt gag gcc aag gag gtt cct ttt tca aac gag aat ccc cga gcg    965
107 Ser Cys Glu Ala Lys Glu Val Pro Phe Ser Asn Glu Asn Pro Arg Ala
108                 140                 145                 150
110 acc gag acc agc cgg ccg agc ctc tcc gag aca ttg ttc cag cga ctg    1013
111 Thr Glu Thr Ser Arg Pro Ser Leu Ser Glu Thr Leu Phe Gln Arg Leu
112             155                 160                 165
114 caa agc atg gac acc agt ggg ctt cca gaa gag cat ctt aag gcc atc    1061
115 Gln Ser Met Asp Thr Ser Gly Leu Pro Glu Glu His Leu Lys Ala Ile
116             170                 175                 180
118 caa gat tat tta agc act cag ctc gcc cag gac tct gaa ttt gtg aag    1109
119 Gln Asp Tyr Leu Ser Thr Gln Leu Ala Gln Asp Ser Glu Phe Val Lys
120     185                 190                 195
122 aca ggg tcc agc agt ctt cct cac ctg aag aaa ctg acc aca ctg ctc    1157
123 Thr Gly Ser Ser Ser Leu Pro His Leu Lys Lys Leu Thr Thr Leu Leu
124 200                     205                 210                 215
126 tgc aag gag ctc tat gga gaa gtc atc cgg acc ctc cca tcc ctg gag    1205
127 Cys Lys Glu Leu Tyr Gly Glu Val Ile Arg Thr Leu Pro Ser Leu Glu
128                 220                 225                 230
130 tct ctg cag agg tta ttt gac cag cag ctc tcc ccg ggc ctc cgt cca    1253
131 Ser Leu Gln Arg Leu Phe Asp Gln Gln Leu Ser Pro Gly Leu Arg Pro
132             235                 240                 245
134 cgt cct cag gtt cct ggt gag gcc aat ccc atc aac atg gtg tcc aag    1301
135 Arg Pro Gln Val Pro Gly Glu Ala Asn Pro Ile Asn Met Val Ser Lys
136         250                 255                 260
138 ctc agc caa ctg aca agc ctg ttg tca tcc att gaa gac aag gtc aag    1349
139 Leu Ser Gln Leu Thr Ser Leu Leu Ser Ser Ile Glu Asp Lys Val Lys
140     265                 270                 275
142 gcc ttg ctg cac gag ggt cct gag tct ccg cac cgg ccc tcc ctt atc    1397
143 Ala Leu Leu His Glu Gly Pro Glu Ser Pro His Arg Pro Ser Leu Ile
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144 280                 285                 290                 295
146 cct cca gtc acc ttt gag gtg aag gca gag tct ctg ggg att cct cag    1445
147 Pro Pro Val Thr Phe Glu Val Lys Ala Glu Ser Leu Gly Ile Pro Gln
148                 300                 305                 310
150 aaa atg cag ctc aaa gtc gac gtt gag tct ggg aaa ctg atc att aag    1493
151 Lys Met Gln Leu Lys Val Asp Val Glu Ser Gly Lys Leu Ile Ile Lys
152                 315                 320                 325
154 aag tcc aag gat ggt tct gag gac aag ttc tac agc cac aag aaa atc    1541
155 Lys Ser Lys Asp Gly Ser Glu Asp Lys Phe Tyr Ser His Lys Lys Ile
156                 330                 335                 340
158 ctg cag ctc att aag tca cag aaa ttt ctg aat aag ttg gtg atc ttg    1589
159 Leu Gln Leu Ile Lys Ser Gln Lys Phe Leu Asn Lys Leu Val Ile Leu
160     345                 350                 355
162 gtg gaa aca gag aag gag aag atc ctg cgg aag gaa tat gtt ttt gct    1637
163 Val Glu Thr Glu Lys Glu Lys Ile Leu Arg Lys Glu Tyr Val Phe Ala
164 360                 365                 370                 375
166 gac tcc aaa aag aga gaa ggc ttc tgc cag ctc ctg cag cag atg aag    1685
167 Asp Ser Lys Lys Arg Glu Gly Phe Cys Gln Leu Leu Gln Gln Met Lys
168                 380                 385                 390
170 aac aag cac tca gag cag ccg gag ccc gac atg atc acc atc ttc atc    1733
171 Asn Lys His Ser Glu Gln Pro Glu Pro Asp Met Ile Thr Ile Phe Ile
172                 395                 400                 405
174 ggc acc tgg aac atg ggt aac gcc ccc cct ccc aag aag atc acg tcc    1781
175 Gly Thr Trp Asn Met Gly Asn Ala Pro Pro Pro Lys Lys Ile Thr Ser
176             410                 415                 420
178 tgg ttt ctc tcc aag ggg cag gga aag acg cgg gac gac tct gcg gac    1829
179 Trp Phe Leu Ser Lys Gly Gln Gly Lys Thr Arg Asp Asp Ser Ala Asp
180     425                 430                 435
182 tac atc ccc cat gac att tac gtg atc ggc acc caa gag gac ccc ctg    1877
183 Tyr Ile Pro His Asp Ile Tyr Val Ile Gly Thr Gln Glu Asp Pro Leu
184 440                 445                 450                 455
186 agt gag aag gag tgg ctg gag atc ctc aaa cac tcc ctg caa gaa atc    1925
187 Ser Glu Lys Glu Trp Leu Glu Ile Leu Lys His Ser Leu Gln Glu Ile
188             460                 465                 470
190 acc agt gtg act ttt aaa aca gtc gcc atc cac acg ctc tgg aac atc    1973
191 Thr Ser Val Thr Phe Lys Thr Val Ala Ile His Thr Leu Trp Asn Ile
192             475                 480                 485
194 cgc atc gtg gtg ctg gcc aag cct gag cac gag aac cgg atc agc cac    2021
195 Arg Ile Val Val Leu Ala Lys Pro Glu His Glu Asn Arg Ile Ser His
196         490                 495                 500
198 atc tgt act gac aac gtg aag aca ggc att gca aac aca ctg ggg aac    2069
199 Ile Cys Thr Asp Asn Val Lys Thr Gly Ile Ala Asn Thr Leu Gly Asn
200     505                 510                 515
202 aag gga gcc gtg ggg gtg tcg ttc atg ttc aat gga acc tcc tta ggg    2117
203 Lys Gly Ala Val Gly Val Ser Phe Met Phe Asn Gly Thr Ser Leu Gly
204 520                 525                 530                 535
206 ttc gtc aac agc cac ttg act tca gga agt gaa aag aaa ctc agg cga    2165
207 Phe Val Asn Ser His Leu Thr Ser Gly Ser Glu Lys Lys Leu Arg Arg
208             540                 545                 550
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210 aac caa aac tat atg aac att ctc cgg ttc ctg gcc ctg ggc gac aag   2213
211 Asn Gln Asn Tyr Met Asn Ile Leu Arg Phe Leu Ala Leu Gly Asp Lys
212             555                 560                 565
214 aag ctg agt ccc ttt aac atc act cac cgc ttc acg cac ctc ttc tgg   2261
215 Lys Leu Ser Pro Phe Asn Ile Thr His Arg Phe Thr His Leu Phe Trp
216             570                 575                 580
218 ttt ggg gat ctt aac tac cgt gtg gat ctg cct acc tgg gag gca gaa   2309
219 Phe Gly Asp Leu Asn Tyr Arg Val Asp Leu Pro Thr Trp Glu Ala Glu
220         585                 590                 595
222 acc atc atc caa aaa atc aag cag cag cag tac gca gac ctc ctg tcc   2357
223 Thr Ile Ile Gln Lys Ile Lys Gln Gln Gln Tyr Ala Asp Leu Leu Ser
224 600                 605                 610                 615
226 cac gac cag ctg ctc aca gag agg agg gag cag aag gtc ttc cta cac   2405
227 His Asp Gln Leu Leu Thr Glu Arg Arg Glu Gln Lys Val Phe Leu His
228             620                 625                 630
230 ttc gag gag gaa gaa atc acg ttt gcc cca acc tac cgt ttt gag aga   2453
231 Phe Glu Glu Glu Glu Ile Thr Phe Ala Pro Thr Tyr Arg Phe Glu Arg
232             635                 640                 645
234 ctg act cgg gac aaa tac gcc tac acc aag cag aaa gcg aca ggg atg   2501
235 Leu Thr Arg Asp Lys Tyr Ala Tyr Thr Lys Gln Lys Ala Thr Gly Met
236             650                 655                 660
238 aag tac aac ttg cct tcc tgg tgt gac cga gtc ctc tgg aag tct tat   2549
239 Lys Tyr Asn Leu Pro Ser Trp Cys Asp Arg Val Leu Trp Lys Ser Tyr
240         665                 670                 675
242 ccc ctg gtg cac gtg gtg tgt cag tct tat ggc agt acc agc gac atc   2597
243 Pro Leu Val His Val Val Cys Gln Ser Tyr Gly Ser Thr Ser Asp Ile
244 680                 685                 690                 695
246 atg acg agt gac cac agc cct gtc ttt gcc aca ttt gag gca gga gtc   2645
247 Met Thr Ser Asp His Ser Pro Val Phe Ala Thr Phe Glu Ala Gly Val
248             700                 705                 710
250 act tcc cag ttt gtc tcc aag aac ggt ccc ggg act gtt gac agc caa   2693
251 Thr Ser Gln Phe Val Ser Lys Asn Gly Pro Gly Thr Val Asp Ser Gln
252             715                 720                 725
254 gga cag att gag ttt ctc agg tgc tat gcc aca ttg aag acc aag tcc   2741
255 Gly Gln Ile Glu Phe Leu Arg Cys Tyr Ala Thr Leu Lys Thr Lys Ser
256             730                 735                 740
258 cag acc aaa ttc tac ctg gag ttc cac tcg agc tgc ttg gag agt ttt   2789
259 Gln Thr Lys Phe Tyr Leu Glu Phe His Ser Ser Cys Leu Glu Ser Phe
260     745                 750                 755
262 gtc aag agt cag gaa gga gaa aat gaa gaa gga agt gag ggg gag ctg   2837
263 Val Lys Ser Gln Glu Gly Glu Asn Glu Glu Gly Ser Glu Gly Glu Leu
264 760                 765                 770                 775
266 gtg gtg aag ttt ggt gag act ctt cca aag ctg aag ccc att atc tct   2885
267 Val Val Lys Phe Gly Glu Thr Leu Pro Lys Leu Lys Pro Ile Ile Ser
268             780                 785                 790
270 gac cct gag tac ctg cta gac cag cac atc ctc atc agc atc aag tcc   2933
271 Asp Pro Glu Tyr Leu Leu Asp Gln His Ile Leu Ile Ser Ile Lys Ser
272             795                 800                 805
274 tct gac agc gac gaa tcc tat ggc gag ggc tgc att gcc ctt cgg tta   2981
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275 Ser Asp Ser Asp Glu Ser Tyr Gly Glu Gly Cys Ile Ala Leu Arg Leu
276         810             815             820
278 gag gcc aca gaa acg cag ctg ccc atc tac acg cct ctc acc cac cat     3029
279 Glu Ala Thr Glu Thr Gln Leu Pro Ile Tyr Thr Pro Leu Thr His His
280     825             830             835
282 ggg gag ttg aca ggc cac ttc cag ggg gag atc aag ctg cag acc tct     3077
283 Gly Glu Leu Thr Gly His Phe Gln Gly Glu Ile Lys Leu Gln Thr Ser
284 840             845             850             855
286 cag ggc aag acg agg gag aag ctc tat gac ttt gtg aag acg gag cgt     3125
287 Gln Gly Lys Thr Arg Glu Lys Leu Tyr Asp Phe Val Lys Thr Glu Arg
288             860             865             870
290 gat gaa tcc agt ggg cca aag acc ctg aag agc ctc acc agc cac gac     3173
291 Asp Glu Ser Ser Gly Pro Lys Thr Leu Lys Ser Leu Thr Ser His Asp
292             875             880             885
294 ccc atg aag cag tgg gaa gtc act agc agg gcc cct ccg tgc agt ggc     3221
295 Pro Met Lys Gln Trp Glu Val Thr Ser Arg Ala Pro Pro Cys Ser Gly
296         890             895             900
298 tcc agc atc act gaa atc atc aac ccc aac tac atg gga gtg ggg ccc     3269
299 Ser Ser Ile Thr Glu Ile Ile Asn Pro Asn Tyr Met Gly Val Gly Pro
300     905             910             915
302 ttt ggg cca cca atg ccc ctg cac gtg aag cag acc ttg tcc cct gac     3317
303 Phe Gly Pro Pro Met Pro Leu His Val Lys Gln Thr Leu Ser Pro Asp
304 920             925             930             935
306 cag cag ccc aca gcc tgg agc tac gac cag ccg ccc aag gac tcc ccg     3365
307 Gln Gln Pro Thr Ala Trp Ser Tyr Asp Gln Pro Pro Lys Asp Ser Pro
308             940             945             950
310 ctg ggg ccc tgc agg gga gaa agt cct ccg aca cct ccc ggc cag ccg     3413
311 Leu Gly Pro Cys Arg Gly Glu Ser Pro Pro Thr Pro Pro Gly Gln Pro
312             955             960             965
314 ccc ata tca ccc aag aag ttt tta ccc tca aca gca aac cgg ggt ctc     3461
315 Pro Ile Ser Pro Lys Lys Phe Leu Pro Ser Thr Ala Asn Arg Gly Leu
316         970             975             980
318 cct ccc agg aca cag gag tca agg ccc agt gac ctg ggg aag aac gca     3509
319 Pro Pro Arg Thr Gln Glu Ser Arg Pro Ser Asp Leu Gly Lys Asn Ala
320     985             990             995
322 ggg gac acg ctg cct cag gag gac ctg ccg ctg acg aag ccc gag atg     3557
323 Gly Asp Thr Leu Pro Gln Glu Asp Leu Pro Leu Thr Lys Pro Glu Met
324 1000            1005            1010            1015
326 ttt gag aac ccc ctg tat ggg tcc ctg agt tcc ttc cct aag cct gct     3605
327 Phe Glu Asn Pro Leu Tyr Gly Ser Leu Ser Ser Phe Pro Lys Pro Ala
328             1020            1025            1030
330 ccc agg aag gac cag gaa tcc ccc aaa atg ccg cgg aag gaa ccc ccg     3653
331 Pro Arg Lys Asp Gln Glu Ser Pro Lys Met Pro Arg Lys Glu Pro Pro
332             1035            1040            1045
334 ccc tgc ccg gaa ccc ggc atc ttg tcg ccc agc atc gtg ctc acc aaa     3701
335 Pro Cys Pro Glu Pro Gly Ile Leu Ser Pro Ser Ile Val Leu Thr Lys
336             1050            1055            1060
338 gcc cag gag gct gat cgc ggc gag ggg ccc ggc aag cag gtg ccc gcg     3749
339 Ala Gln Glu Ala Asp Arg Gly Glu Gly Pro Gly Lys Gln Val Pro Ala
```

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date